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(54) Title: COMPOSITIONS, METHODS, KITS AND APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF TARGET MOLECULES (57) Abstract The present invention is directed to methods, compositions, kits and apparatus to identify and detect the presence or absence of target analytes. The embodiments of the present invention have utility in medical diagnosis and analysis of various chemical compounds in specimens and samples, as well as the design of test kits and apparatus for implementing such methods.		

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**COMPOSITIONS, METHODS, KITS AND APPARATUS FOR DETERMINING
THE PRESENCE OR ABSENCE OF TARGET MOLECULES**

FIELD OF THE INVENTION

5 The present invention is directed to methods, compositions, kits and apparatus to identify and detect the presence or absence of target analytes. The embodiments of the present invention have utility in medical diagnosis and analysis of various chemical compounds in specimens and samples, as well as the design of test kits and apparatus for implementing such methods.

10 BACKGROUND OF THE INVENTION

 Molecular biology advances in the last decade gave great promise for the introduction of new, sensitive technologies to identify various analytes in test specimens, including the ability to diagnose cancer, infectious agents and inherited diseases. Clinical molecular diagnostics depend almost exclusively on restriction
15 enzyme analyses and nucleic acid hybridization (Southern and Northern blots) (Meselson and Yuan, 1968, Southern, 1975). Clinical tests based on molecular biology technology are more specific than conventional immunoassay procedures and can discriminate between genetic determinants of two closely related organisms. With their high specificity, nucleic acid procedures are very important tools of molecular
20 pathology. However, nucleic acid procedures have limitations, the most important of which are the procedures consume time, they are labor intensive, and have low sensitivity (Nakamura 1993).

 In any sample, the number of protein molecules of one kind is usually several times higher than the corresponding mRNA, and several hundred times higher than
25 the number of genes encoding them. Using antigen-specific antibodies is a routine procedure in the modern diagnostic industry, although antibody development and purification usually require laborious work. The specificity of tests based on monoclonal antibodies depends on the capacity of antibodies to differentiate between antigens, and might approach the specificity of tests based on nucleic acid
30 hybridization. The sensitivity of these tests, however, is routinely significantly lower than tests based on nucleic acid hybridization, even though the number of protein target molecules in each cell is relatively higher than the nucleic acid molecules corresponding to them. It is desirable to use proteins as the targets in diagnostic tests because of their abundance.

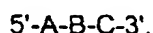
35 Thus, a need exists for improved diagnostic and analytical methods to detect

the presence or absence of target molecules. A need also exists to detect non-nucleic acid analytes with nucleic acid chemistry. And, there is a need to detect protein targets with nucleic acid chemistry coupled to a amplification system.

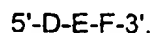
5 SUMMARY OF INVENTION

The present invention features methods, compositions, kits, and apparatus for determining the presence or absence of a target molecule.

One embodiment of the present invention is a composition. The composition comprises a first ribonucleic acid (RNA) molecule and a second RNA molecule. The
10 first RNA molecule is capable of binding to a target molecule and has the following formula:



As used above, A is a section of the RNA molecule having 10-100,000 nucleotides, which section is capable of being received by an RNA replicase and with
15 another RNA sequence, F, being replicated. The letter "B" denotes a section of the RNA molecule having approximately 10 to 50,000 nucleotides, which section is capable of binding to the target molecule. The letter "C" denotes a section of the RNA molecule having approximately 1 to 10,000 nucleotides which section is capable of being ligated to another RNA sequence, "D". The second RNA molecule is capable of
20 binding to a target molecule and has the following formula:



As used above, D is a section of the RNA molecule having approximately 1 to 10,000 nucleotides, which section is capable of being ligated to another RNA sequence, "C". The letter "E" denotes a section of the RNA molecule having
25 approximately 10 to 50,000 nucleotides, which section is capable of binding to the target molecule. The letter "F" denotes a section of the RNA molecule having 10-100,000 nucleotides which section is capable of being received by an RNA replicase and with another sequence, "A", being replicated. The first and the second RNA molecules are capable of forming a third RNA molecule having the following formula:



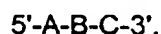
The third RNA molecule is formed by ligation the C and D sections, as the E and the B sections are bound to the target. The third RNA molecule is capable of being received by an RNA replicase and being replicated by such enzyme.

Preferably, the sequences represented by the letters "A" and "F" are selected from the group of sequences consisting of MDV-I RNA, Q-beta RNA microvariant RNA, nanovariant RNA, midivariant RNA and modifications of such sequences that maintain the ability of the sequences to be replicated by RNA replicase. Preferably, the replicase is Q-beta replicase.

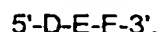
Preferably, the sections B and E each are sections having 10-5,000 nucleotides and, even more preferred, 20-50 nucleotides. Preferably, the sections B and E bind to the target through non-nucleic acid base pairing interactions. And, preferably, the B and E sections are aptamers or partial aptamers as defined by Klug and Famulok (1994). Aptamers are selected for a particular functionality, such as binding to small or large organic molecules, peptides or proteins, the tertiary structure of nucleic acids or complex or simple carbohydrates. The section B and E may be derived from naturally occurring RNA exhibiting affinity for proteins. The sections B and E may also be engineered from computer modeling studies.

Preferably, the sections C and D each have 1-10,000 nucleotides, and more preferred, 1-1000 nucleotides, and most preferred, 1-15 nucleotides. Preferably, the sections C and D, when ligated together, define a recognition site for a ribozyme or a target of another compound that has an endonucleolytic activity against a single-stranded nucleic acid.

A further embodiment of the present invention features a method of determining the presence or absence of a target molecule. The method comprises the steps of providing a first RNA molecule and a second RNA molecule. The first RNA molecule is capable of binding to a target molecule and has the formula:



The sections A, B and C are as previously described. The second RNA molecule is capable of binding to the target molecule and has the formula:



The sections D, E and F are as previously described. The method further comprises the step of imposing binding conditions on a sample potentially containing target molecules in the presence of the first and second RNA molecules. In the presence of the target molecule, the first and the second RNA molecules form a complex with the target molecule. The method further comprises the step of imposing RNA ligase reaction conditions on the sample to form a third RNA molecule in the presence of the target. The third RNA molecule has the formula:

4

5'-A-B-C-D-E-F-3'.

The sample is monitored for the presence of the third RNA molecule, presence or absence of which is indicative of the presence or absence of the target molecule.

Preferably, the sections B and E bind to the target through non-nucleic acid pairing interactions. And, most preferred, the B and E sections are aptamers or partial aptamers.

Preferably the sections C and D together comprise 5-15 nucleotides which define a site for a ribozyme or a target of another compound that has endonucleolytic activity against a single-stranded nucleic acid.

Preferably, at least one of the first or second RNA molecules has a signal generating moiety. After RNA ligase reaction conditions are imposed, the method preferably comprises the further step of separating or enzymatically destroying the RNA molecules unbound with the target molecule and bearing the signal generating moiety.

Preferably, the signal-generating moiety is sections A and F of the third RNA molecule, which sections allow recognition and replication by RNA replicase. Thus, the method further comprises the step of imposing RNA replicase conditions on the sample potentially comprising the third RNA molecule.

A further embodiment of the present invention comprises a kit for determining the presence or absence of a target molecule. The kit comprises one or more reagents comprising a first RNA molecule, a second RNA molecule and an RNA ligase. The first RNA molecule has the formula:

5'-A-B-C-3'.

The second RNA molecule has the formula:

5'-D-E-F-3'.

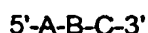
In the presence of the target, the first and the second RNA molecules are capable of forming a target-first-and-second-RNA complex and in the presence of RNA ligase means forming a third RNA molecule having the formula:

5'-A-B-C-D-E-F-3'.

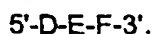
The letters A, B, C, D, E, and F are as previously described. The third RNA molecule is preferably capable of being received and replicated by RNA replicase.

Preferably, the kit further comprises reverse transcriptase and suitable primers.

An embodiment of the present invention further comprises a method of making a first RNA molecule and a second RNA molecule, wherein the first RNA molecule has the formula:

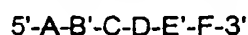


5 and the second RNA molecule has the formula:



As used above, the letters A, B, C, D, E, and F are as previously described, and the sections C and D together define a site for cleavage by ribozyme or another compound having endonucleolytic activity against a single-stranded nucleic acid.

10 The method comprises the step of combining a sample containing the target molecule with a library of RNA molecules having the formula:



to form a mixture of one or more target bound-RNA molecules and one or more unbound-RNA molecules. The letters B' and E' represent potential sections B and E.

15 Preferably, the sections B' and E' are randomized nucleotides.

Optionally, as an alternative, primer nucleic acid corresponding to at least one section is added to the mixture with an enzyme capable of degrading the unbound RNA molecules. However, this step may be omitted and the bound RNA molecules amplified as set forth is the next step.

20 Next, bound RNA molecules are released from the target and amplified with RNA replicase, and preferably Q-beta replicase, to form an amplification product. This amplification product can be serially diluted and amplified, repeatedly if needed, to identify a preferred amplification product. Next, the RNA molecules comprising the amplification product having the formula:



are cleaved to form the first and second RNA molecules.

Preferably, the cleavage is performed with a ribozyme or other endonucleolytic enzyme and the sections C and D together define a cleavage site for the ribozyme or another endonucleolytic enzyme.

30 Preferably the step of degrading the unbound RNA molecules is performed in the presence of the enzyme reverse transcriptase. Preferably, the step of amplifying the bound RNA molecules is performed in the presence of the enzyme Q-beta replicase.

An embodiment of the present invention further comprises a kit for performing the above method of identifying first and second RNA molecules. The kit comprises one or more nucleic acid molecules having sections corresponding to the sections A, B, C, D, E, and F. Preferably, the kit comprises sections B' and E' as randomized nucleotide sequences.

As used herein the term "kit" refers to an assembly of parts, compositions and reagents with suitable packaging materials and instructions.

The present invention is further described in the following figure and examples, which illustrate features and highlight preferred embodiments and the best mode to make and use the invention.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1 depicts plasmid pT7 MDV-XhoI. This plasmid was used for cloning synthesized PX and XS dsDNAs and for the transcription of the PX and XS recombinant RNA molecules that served as detector molecules for adenovirus sequences;

Figure 2 depicts a hybridization product; and

Figure 3a and 3b depict a an affinity product and a ligation product.

DETAILED DESCRIPTION OF INVENTION

The present invention will be described with respect to a SELEX process and Q-beta technology. SELEX processes are described more fully in several references (King and Famulok, 1994) (Ellington and Szostak, 1990) and (Gold et al 1995). The method features the incorporation of specially-designed RNA libraries into a Q-beta replicase template. The methods of the present invention are more effective than other methods known in the art for several reasons.

First, Q-beta replicase can only use templates with high structural complexity, which are the best candidates for aptamers with great affinity for the target molecule. The original library is pre-selected for the species with secondary and tertiary structures when the original library of randomized sequences is amplified with Q-beta replicase prior to its contact with the target molecule.

Secondly, the special design of the libraries will allow amplification of the high affinity ligands by enzymatic degradation of the low affinity molecules discriminately

and selectively without an elaborate process of partitioning them from ligands of low affinity.

Thirdly, amplification of the ligands by Q-beta replicase as a part of the chimeric template RNA seems more manageable technically and more time advantageous than using routine PCR techniques during standard SELEX procedures.

Finally, Q-beta chimeric RNA template with an insert of RNA ligands highly specific for a target protein can serve directly as a unique tool to detect in clinical specimens target molecules having tertiary configurations.

The embodiments of the invention have application for constructing specially designed nucleic acid detector molecules for any analytes, including proteins, that naturally exhibit an affinity for nucleic acid molecules and, especially, RNA molecules. The methods, compositions and kits have utility in the study of RNA-protein interactions and their significance in regulatory systems, for diagnosis of cancer, infectious and inherited diseases. The list of naturally-occurring and medically-important RNA-protein complexes includes, but is not limited to, RNA-binders of bacteria and parasites, intron binding proteins, RNA epitopes in autoimmune diseases, protein-nucleic acid complexes of spinal muscular atrophy or in fragile-X mental retardation and RNA-protein subunits in telomerase. Naturally occurring nucleoprotein complexes also include any regulatory proteins, enzymes, antibodies, antibiotics and other complex chemical compounds, as well as simpler complexes, such as nucleotides, nucleosides or amino acids and such, for which naturally-occurring nucleic acid ligands have been identified and described. The proposed method is also useful for any target molecule for which nucleic acid ligands were obtained through SELEX, *in vitro* selection or *in vitro* evolution procedures.

The embodiments of the present invention feature a method for constructing the sets of two detector molecules for identifying various analytes different from nucleic acid targets in a specimen. The composition of the detector molecules is based on a ligand's nucleotide sequences, and the secondary and tertiary structure of the ligand corresponding to such target analyte. The detector molecules mean two RNA molecules that serve three purposes: to be a ligand with high affinity to the target analyte, to be ligated into one functional molecule, and to be a template that could be amplified by Q-beta replicase after its ligation by RNA ligase. The specimen means any sample taken from any source and preferably, from biological sources. Target

analyte means any compound of interest without limitation. Ligand means a nucleic acid molecule that demonstrates high affinity to the target analyte.

One embodiment of the present invention features a method for designing and constructing two detector molecules representing the nucleic acid component of a nucleoprotein complex molecule or a ligand of known nucleotide sequence. The detector molecules are constructed through cloning them as appropriate oligonucleotides in the recombinant plasmid using a Q-beta replicase template cDNA insert or synthesizing them on a DNA synthesizer, or using PCR techniques.

To construct the detector molecules for a target analyte with a known ligand, two sets of complementary oligonucleotides are designed and synthesized on a DNA synthesizer. One set of oligonucleotides is dsDNA representing the 5' part of the whole ligand. The other set of oligonucleotides is dsDNA representing the 3' part of the same ligand. Both dsDNAs are designed with terminal restriction enzyme sites for cloning in the vector, and with additional nucleotides with lengths from one to ten nucleotides. These additional sequences will be used in subsequent steps of the procedure to synthesize captomers (from Lat. *capere* - seek to get), parts of the molecules with a specially-designed function. The first dsDNA has the following formula: M-N-O-P. The second dsDNA has the following formula: P-R-S-T, where M, P and T are restriction site linkers, O is sequences representing the 5' segment of the ligand, R is sequences representing the 3' segment of the ligand, and N and S are the sequence with donor and acceptor termini employed in a ligation reaction.

These two dsDNAs are cloned in a recombinant plasmid containing T7 RNA promoter, followed immediately by inserting a Q-beta replicase template cDNA (Fig. 1). Three unique restriction sites (M, P and T) for cloning dsDNA molecules are incorporated into the recombinant plasmid. One cloning site, M follows the T7RNA promoter immediately. The T cloning site is inserted into the end of the Q-beta replicase template, and the P site divides the template insert into two, 5' and 3', parts. Thus, the 5' part of the Q-beta replicase template is flanked by M and P restriction sites and 3' part of the template is flanked by P and T restriction sites.

The composition of the insert in such recombinant plasmid will be :

T7 promoter-M-Q-beta template-P-Q-beta template-T

A second recombinant plasmid is prepared by replacing the 5' part of the Q-beta replicase template cDNA situated between the M and P restriction sites with

corresponding dsDNA representing the 5' segment of the ligand. The combined insert of the second recombinant plasmid has the following formula:

T7 promoter-M-N-O-P-Q-beta template-T.

A third recombinant plasmid is prepared by replacing the 3' part of the Q-beta replicase template cDNA situated between the P and T restriction sites with
5 corresponding dsDNA representing the 3' segment of the ligand. The combined insert of the third recombinant plasmid has the formula:

T7 promoter-M-Q-beta template-P-R-S-T.

Recombinant plasmids containing the template sequences with the inserted
10 sequences are used to transform competent bacterial cells, and the transformed cells are grown in a culture. The cultured cells are harvested and lysed. The DNA plasmids are purified. In the said method for design and construction of the first and second detector-molecules, the recombinant plasmids are cleaved with an appropriate restriction enzyme and the recombinant Q-beta replicase templates containing the
15 inserts are transcribed into the RNA using T7 RNA promoter. All procedures are performed according to the standard protocols of Sambrook et al., (1989) known to someone skilled in the field of molecular biology.

The second and third recombinant plasmids will be linearized by cleavage in the T restriction site, and the recombinant RNAs will be transcribed from each plasmid
20 using the T7 RNA promoter.

Two recombinant RNA transcripts are the set of detector-molecules for the chosen analyte.

Each such RNA detector-molecule consists of three segments.
The structure of the first detector-molecule is:

25 5'-A-B-C-3'.

And the structure of the second detector-molecule is:

5'-D-E-F-3'.

Each component has one defined function—amplification, recognition or ligation. The A and F "amplification" segments of the first and second detector-molecules are parts of a template replicable by Q-beta replicase. The nucleotide
30 composition and the length of the A and F segments depends on the replicable RNA they represent. Preferably, segments A and F are selected from the group of replicable RNAs consisting of MDV-I RNA, Q-beta RNA, microvariant RNA, midivariant RNA, nanovariant RNA, or modifications thereof that permit the RNA to

10

maintain its reproducibility. Neither the A nor the F parts of the Q-beta template can separately serve for amplification by Q-beta replicase.

A preferred sequence for section A is set forth in SEQ ID No. 1 below:

5

SEQ ID No. 1

5'-GGGGACCCCC CCGGAAGGGG GGGACGAGGU GCGGGCACCU
CGUACGGGAG UUCGACCGU GACGCUCUAG-3'

A preferred sequence for section F is set forth in SEQ ID No. 2 below:

10

SEQ ID No. 2

5'-AGAUCUAGAG CACGGGCUAG CGCUUUCGCG CUCUCCCAGG
UGACGCCUCG UGAAGAGGCG CGACCUUCGU GCGUUUCGGU
GACGCACGAG AACCGCCACG CUGCUUCGCA GCGUGGCUCC
UUCGCGCAGC CCGCUGCGCG AGGUGACCCC CCGAAGGGGG
GUUCCC-3'

15

Sequences Nos. 1 and 2 are the sequences of MDV-1 RNA template for Q-beta replicase.

In the alternative, a preferred sequence for section A is set forth in SEQ ID No.3 below:

20

SEQ ID No. 3

5'-GGGGAAAUCC UGUUACCAGG AUAACGGGGU UUCCUCA-3'

And, a preferred sequence for section F is set forth in SQ ID No. 4 below:

25

SEQ ID No. 4

5'-CCUCUCUACU CGAAAGUUAG AGAGGACACA CCCGGAUCUA
GCCGGGUCAA CCCA-3'

30

The B and E "recognition" segments represent the full length or part of two ligands with high affinity to two epitopes of the same analyte, or, they are two parts of a single nucleic acid ligand with high affinity to a single epitope of the target analyte or nucleic acid component of the nucleoprotein complex. Segments B and E are the RNA transcripts of the R and O parts of the ligand described above.

The D and C "ligation" segments termed *captomers* (from Lat. *capere* - seek to get) are segments of the detector molecules, with specially-designed donor and acceptor terminal nucleotides that are essential for ligating the two detector molecules after they bind with the target molecules, the termini of which are used by RNA ligase in the ligation reaction to form phosphodiester bonds. The lengths of these segments can be as short as one nucleotide and as long as 10,000 nucleotides. These two segments are the RNA transcripts of the captomer parts N and S of the recombinant dsDNA molecules. Neither of these two recombinant RNA molecules can separately serve as a template for Q-beta replicase.

The synthesis of dsDNA, the cloning and the transcription of the recombinant RNA molecules are performed under the conditions described in detail (Sambrook et al., 1989) and known to someone skilled in the field of molecular biology.

Another embodiment of the present invention features a method for designing and constructing a pair of detector-molecules for any three-dimensional analyte when the nucleotide sequence of its ligand is not known. The method comprises the steps of providing a first detector-molecule and a second detector-molecule.

Preferably, the process starts from constructing machine-synthesized libraries of deoxyribonucleotides. Each member of each library is composed of at least the four segments:

Where the B and E segments are approximately 5'-B-CD-E-X-3', 10-50,000 nucleotides and, most preferably, 20-50 nucleotides each, and the CD segment is of 1 to 10,000 nucleotides and, most preferably, 2-30 sequences, and X is 10-15 nucleotides long.

Preferably, the B and E segments are random nucleotide sequences where A, T, C and G nucleotides have an equal probability to be incorporated in any position of the segment. Each member of the synthesized library is different from others in these two regions.

Preferably, the C-D segment contains DNA sequences that are a recognition site for a known ribozyme defined and described by O. Uhlenbeck (1987) as well as by GF Joyce (1989), TR Cech, FL Murphy, AJ Zaug, C. Grosshans, US Patent No 5,116,742 (1992), JP Hazeloff, WL Gerlach, PA Jennings, FH Cameron, US Patent No 5,254,678 (1993), HD Roberson and AR Goldberg US Patent No 5,225,337 (1993) or any other compound that demonstrates a specific endonucleolytic activity with single-stranded nucleic acid molecules. The segment with ribozyme recognition

sequences is identical in all molecules of the same library, but varies among the libraries.

Preferably the X segment is a DNA oligonucleotide segment with random, but defined sequences. Each molecule of the synthesized library has the same X region.

5 The single-stranded original library will be converted into a double-stranded DNA library using any DNA polymerase that includes, but is not limited to DNA polymerase I, Klenow fragment, T4 DNA polymerase, T7 DNA polymerase, and primers complementary to the X section of the synthesized molecules. The conversion of the ssDNA library into a dsDNA library, primer and enzymes is
10 performed under standard conditions known to someone skilled in the field of molecular biology.

The dsDNA library is cloned into a recombinant plasmid (similar to the one described previously, Fig. 1) containing the T7 RNA transcription promoter attached to a cDNA copy of the Q-beta replicase template with an insert of a unique restriction
15 enzyme linker within the sequence of whole recombinant plasmid, including the Q-beta replicase template. Insertion of the library sequences into the Q-beta template at the position chosen must not unduly perturb the features of the template necessary for successful amplification. Insertion of the dsDNA library into a recombinant plasmid containing a cDNA copy of Q-beta replicase template is performed under standard
20 conditions known to someone skilled in the field of molecular biology.

Recombinant plasmids containing the template sequences with the inserted sequences from the original DNA library are used to transform competent bacterial cells, and the transformed cells are grown in a culture. The cultured cells are harvested and lysed. The DNA plasmids are purified. In the said method for design
25 and construction of the first and second detector-molecules, the recombinant plasmids are cleaved with an appropriate restriction enzyme and the recombinant Q-beta replicase templates containing the inserts of the original DNA library are transcribed into the RNA library using T7 RNA promoter. All procedures are performed according to the standard protocols of Sambrook et al., (1989) known to someone skilled in the
30 field of molecular biology.

Composition of each species of the second RNA transcripts library, is 5'-A-B-C-D-E-F-3'.

Each species is a molecule with three functional parts. The A and F are two parts of a single Q-beta template and enable amplification of the whole detector

molecule. The B and E segments represent random sequences of the library in the recombinant RNA transcript. The CD segment of each RNA transcript is a joining region of the B and E sequences and contains a recognition site for a chosen ribozyme or any other compound that demonstrates the cleavage of the single-stranded nucleic acid-specific sequences. The X segment is not essential for further procedures and it is not described in further descriptions.

A further embodiment of the present invention describes a method of enrichment of the original RNA library with RNA species that demonstrate secondary and tertiary complexity in the B and E regions. The recombinant transcript-RNAs' library templates are used to initiate amplification in a standard Q-beta replicase reaction according to the standard procedure described in detail by Axelrod et al., (1991). The secondary structure of the RNA templates has a very powerful influence on replication by the Q-beta enzyme. In fact, the existence and continual propagation of whole recombinant RNA species as self-replicating entities depends on these structures as the major factor in determining the viability of the amplification products. Q-beta replicase discriminates the inserts as a part of the template molecule on the basis of their secondary structures and provides a positive selection favoring those templates containing inserts with more complex secondary structures, as follows from Axelrod et al., (ibid.). Thus, after several, preferably three or four, cycles of replicating with Q-beta replicase, the library of recombinant RNA templates will be "preselected" for those recombinants with a higher proportion of the complex secondary structures that result from nucleotide pairing and interaction.

Additionally, the "preselection" process for spatial complexity of B and E region will lead to an additional diversity of the original RNA library. Since Q-beta replicase can use both, plus and minus strands of RNA as templates, the "preselected" library will consist of two types of molecules that are plus and minus versions of the same sequence.

The secondary structure motifs contain such elements as pseudo knots, simple stems or hairpins, or stems with loops, or symmetrical and asymmetrical bulges and such. Double-stranded RNA of the B-CD-E part with motifs of secondary structure in turn form a three dimensional structure, the tertiary structure of the recombinant RNA in this region, converting the B and E segments into segments with randomized three-dimensionally-structured nucleotide sequences. The relationship between nucleotide sequences in RNA molecules, and secondary and tertiary organization of RNA

molecules is described in detail by L. Gold and C. Tuerk, US Patent No. 5,475,096 (1995).

The further embodiment of the present invention features a procedure for selecting recombinant RNA species that demonstrate high affinity to a target molecule of particular functionality, such as binding to small or large organic and non-organic molecules with their own tertiary structures, including peptides or proteins, nucleic acid molecules or oligonucleotides, nucleotides or amino acids, complex or simple vitamins, antibiotics and carbohydrates and such without limitation. The procedure comprises the steps of contacting the library with the target molecules, providing an annealing of the detector-molecules preselected for tertiary structure with a population of the said target molecules under conditions favorable for forming the complex between the chosen target and recombinant RNA molecules. The annealing will be performed under favorable conditions described by Gold et al., (1995). Specifically, the recombinant RNA molecules will form a binding complex with the target molecule in the 5'-B-CD-E-3' region, and particularly, in the B and E segments. Preferably, sections B and E bind through non-nucleic acid base pairing interaction to the analyte. These two segments may anneal to the same "epitope" of the target molecule, acting as two parts of a single nucleic acid ligand or, as an alternative, the B and E segments can act as two separate ligands forming bonds with two separate "epitopes" of the same target molecule. The CD region may or may not participate in the annealing with the target molecule, depending on its nucleotide constitution, nature of the target molecule and its interaction with the B and E segments.

Several possible configurations of molecules are in the mixture after completing an annealing reaction: free RNA species, free target molecules and RNA/target molecule complexes. Additionally, RNA/target molecules complexes can be formed by annealing both B and E segments to the analyte molecules, or either of them, B or E, annealed to the analyte molecule separately. Several methods suggested for partitioning the free RNA species from the target/RNA complexes, including filter binding, gel mobility shift, affinity chromatography, antibody precipitation, phase partitioning and protection from nucleolytic cleavage by catalytic RNAs, termed ribozymes, have been described in detail by L. Gold and C Tuerk, US Patent No. 5,475,096 (1995). Further, L. Gold and S. Rinquist, US Patent No. 5,567,588 (1996) widened the methods that should be employed for partitioning nucleic acid molecules annealed to the target analyte from those that do not bind the target molecules. Their

new method, termed solution SELEX, employs a primer extension inhibition, exonuclease hydrolysis inhibition, linear to circular formation, and single stranded nucleic acid PCR amplification for the partitioning between high- and low-affinity nucleic acid-target complexes.

5 Preferably, the third RNA molecules are amplified by Q-beta replicase. The amplification product is serially diluted and subjected to additional amplification to render the unbound, unamplified nucleic acids as mere background. This step of dilution and amplification can be repeated until the one or more desired nucleic acids are present in a concentration much greater than any other components. However,
10 additional selection steps may be applied as described below.

A further embodiment of the present invention is based on the enzymatic selection of the recombinant RNA template with high affinity to target molecules of the B-CD-E region embedded between two sectors, A and F, of the Q-beta template. To initiate this selection, we use a reverse transcriptase (RT), preferably Avian
15 myeloblastoma virus (AMV) reverse transcriptase and an RT primer with nucleotide sequences complementary to a segment of CD region. Reverse transcriptase from avian myeloblastosis virus is a DNA polymerase that catalyzes polymerization of nucleotides using an RNA template. This enzyme consists of two polypeptide subunits, one of which contains 5'-3' polymerase activity and the other a powerful
20 RNase H activity (Verma, 1991). Reverse transcriptase has been widely used to synthesize complementary DNA (cDNA). Such synthesis requires a primer and free nucleotides. The RT enzyme will synthesize cDNA and simultaneously degrade the complementary RNA molecule because of its RNase H activity. RNA with high affinity to the target analyte molecule will be protected from degradation due to the fact that
25 the primers do not bind and RT cannot synthesize cDNA. Therefore RNase H has no activity.

The dissociation constant of the high affinity detector RNA-target analyte complex is in the nanomolar-or-less range and efficiently inhibits annealing of the primer with complementary sequences of the C and D regions bound to two separate
30 epitopes or with one epitope, and, possibly, in configuration when only the C or D region is bound to a single epitope. The success of the RT primer annealing with the RNA molecule in the latter configuration will depend on the energy balance between the epitope-RNA and the primer-RNA complexes. At the same time, the RT primer will anneal efficiently with the complementary sequences of the CD region of the free

recombinant RNA molecule. As a result, reverse transcriptase synthesizes the cDNA strand using the free recombinant RNA molecule only, and in those RNA-target complexes where the energy balance shifts in a direction favorable for creating a primer-RNA complex. In the process of synthesizing cDNA, reverse transcriptase
5 degrades the original RNA in RNA-DNA hybrids exonucleolytically because it has RNase H activity. Thus, a large section of the recombinant RNA molecules with low affinity to the target, starting from the CD section to the end of the whole RNA recombinant molecule will be degraded. As a result, all low affinity and partially annealing to the analyte RNA molecules will be eliminated from the amplifiable pool,
10 and only completely annealing with target analyte recombinant RNA molecules with high affinity for the B-CD-E region will represent the pool amplifiable by a Q-beta replicase template.

Using enzymatic degradation of RNA molecules with low affinity to the target by RNase H allows isolation and consequent dissociation of the high affinity RNA-target
15 molecules complex and purification of the high affinity RNA molecule(s) from the target molecules. Purification of the whole-length recombinant RNA molecules from the target is performed in conditions favorable for each target-RNA molecule combination. Purified RNA recombinant molecules with high affinity to the target are amplified by Q-beta replicase, using the standard protocol described further in the
20 EXAMPLE section.

A further embodiment of the present invention features the procedures for producing detector molecules from the product of the described enzymatic degradation of low affinity RNA species and propagation of recombinant RNA molecules that demonstrate high affinity to the chosen target analyte. All members of
25 the remaining population will be exposed to an appropriate ribozyme or another agent that specifically cleaves the CD sequence. Each RNA molecule will be split into two molecule-detectors. The first molecule-detector will be composed of the sectors 5'-A-B-C-3'. The second molecule detector will have the order of the segments comprising it as 5'-D-E-F-3'. The function of each segment was described earlier, except that
30 each of the detector molecules will have a new component—a terminal C or D region that was previously united in the CD region of the transcribed recombinant RNA molecule. These two regions acquire a new important function in the detector-molecules and will serve as the donor-acceptor captomers, the parts of the ligation complex.

The constructed set of two detector molecules is ready for use in detecting target analytes in clinical specimens.

In a modified variant, the detector molecules are ssDNA molecules with the composition of the segments similar to those of the RNA nature. Both detector molecules contain the sequences representing the two parts of the Q-beta replicase template, the detection parts with high affinity to the analyte molecule and the sequences recognizable by a DNA endonuclease. One of the detector molecules further includes an RNA polymerase promoter sequence to enable transcription of the DNA detector-molecules annealed to the target and ligated into a recombinant RNA molecule. The organization of such recombinant RNA is the same as was described previously, that is, restriction enzyme sequences are flanked by two analyte recognition sequences and those sequences are flanked by Q-beta replicase template sequences. This recombinant RNA molecule is a template that will be amplified by Q-beta replicase.

A further embodiment of the present invention features the procedures for detection of an analyte molecule in a specimen using a constructed set of detector molecules. The constructed detector molecules could be used in diagnostic tests, in diagnostic test kits and for microensors or nucleic acid biochip production. For detection of an analyte molecule, a mixture of two detector-molecules is combined with a specimen potentially containing the target analyte. The target, when present in the specimen, will bind the detector-molecules, and the two halves of the original recombinant RNA molecule will be situated on the target analyte in such a position that they can be ligated with RNA ligase. After ligation, which occurs between the 3' and 5' terminal nucleotides of the C and D sectors, the two detector molecules form a single molecule. Such molecules that combine the A and F sectors of the detector molecules, can serve as a template for Q-beta replicase. Template ability is restored after ligation of the detector molecules into a single reporting recombinant template molecule that can then be amplified by Q-beta replicase.

Preferably, the two RNA detector- probes are joined or ligated when bound to the target by an enzyme. One such enzyme be RNA ligase, and preferably T4 RNA ligase, originally described by Leis et al., (1972). Similarly to DNA ligase, T4 RNA ligase catalyzes the formation of a 3'→5' phosphodiester bond between a 3'-terminal hydroxyl and a 5'-terminal phosphate of polyribonucleotides with hydrolysis of ATP to AMP and Ppi (Silber et al., 1972). The circularization reaction of the oligonucleotides

by T4 RNA ligase provides some information on the optimum physical distance between the donor and acceptor parts of an RNA molecule, the optimum of which varies between a distance of 10-16 nucleotides (Kaufmann et al., 1974, Sugino et al., 1977). The major feature that differs RNA ligase from DNA ligases is that RNA ligase aligns the free ends of the reacting donor and acceptor on its surface, whereas DNA ligase requires a base-paired template that fixes the oligonucleotide ends in close proximity (Engler and Richardson, 1982, Uhlenbeck and Gumpert, 1982).

To create the optimal conditions for the RNA ligase, the claimed set of detector-molecules is designed with the option to bind the target analyte with a gap between them. Additionally, each of the detector-molecules is designed with terminal nucleotides that should be free in a detector-analyte complex. Neither of these new structural components in the claimed detector-target complexes exists in standard nucleic acid probe-nucleic acid target complexes.

Preferably the RNA molecules do not align contiguously with each another on the target or on the analyte forming a gap between 20 and 200 angstroms. Additionally, the RNA molecules align on the target or on the analyte with free termini, that do not hybridize to the target molecule or bind to the analyte.

Another embodiment of the present invention is the composition of the two detector-molecules that work in conjunction with each other when they are used in diagnostic protocols, kits or apparatus. Each of the detector-molecules consists of three functional parts. One of them is a segment of Q-beta replicase template, another is a segment of the sequence with high affinity to the target, and the third part is a segment of the sequences with the recognition site for a chosen endonucleatic compounds which, after the cleavage, acquires a captomer's function. The first detector molecule is capable of binding to the target molecule and has the following formula, with at least three components organized in a 5'->3' direction as:

5'-A-B-C-3'.

As used above, A is a section of the first detector molecule having the 5' section of a Q-beta replicase template, which is not capable of binding to the target molecule and which is not capable of replication. The letter B denotes a section of approximately 20 to 50 nucleotides of the first detector-molecule which is the section capable of binding to the target molecule. The letter C denotes a captomer, a section of the first detector composed of approximately 1 to 15 nucleotides, which is the

primary substrate for a ribozyme. The C captomer can and cannot be capable of binding to the target molecule.

The second detector-molecule is capable of binding to the target molecule and has the following formula with at least three components organized in a 5'→3' direction as:

5'-D-E-F-3'

As used above, the letter D denotes a captomer, a section of the second detector composed of approximately 1 to 15 nucleotides, which is another primary substrate for a ribozyme. The D captomer can and cannot be capable of binding to the target molecule. The letter E denotes a section of the second detector-molecule having approximately 20 to 50 nucleotides which section is capable of binding to the target molecule in the same "epitope" as sector B of the first detector molecule or to its own "epitope". The F part of the second detector-molecule contains the remaining 3' section of a Q-beta replicase template. The A and F segments are not capable of binding to the target molecule and cannot be amplified separately by Q-beta replicase.

Preferably, sections C and D are the nucleotide sequences, termed *captomers*, that can serve as a donor, since section C naturally terminates in the hydroxyl group required for ligation, and, section D, that can serve as an acceptor, with a terminal monophosphate group required by the ligation reaction catalyzed by RNA ligase, which includes but is not limited to bacteriophage T4 DNA ligase. The ligation reactions are performed under standard conditions known to those skilled in the field of molecular biology.

Preferably, upon ligation of sections C and D the two detector-molecules form a single molecule composed of five parts in the 5'-3' order

5'-A-B-C-D-E-F-3'

as in the original recombinant RNA demonstrating high affinity to the target molecule.

Preferably, the newly formed molecule is a template amplifiable by Q-beta replicase and has a signal-generating moiety. Signal-generating moieties comprise, by way of example, radiolabeled nucleotides, enzymes, ligands, fluorescent or chemoluminescent agent, or sequences of nucleotides capable of detection. A preferred signal-generating moiety is section A of the first detector molecule and section F of the second detector-molecule, which are two sections of the replicable nucleic acid template. And, most preferably, sections A and F are selected from the naturally-occurring group of replicable RNAs consisting of MDV-I RNA, Q-beta RNA,

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microvariant RNA, midvariant RNA, nanovariant RNA and modifications thereof, or any artificially constructed RNA templates that permit the RNA to maintain replicable RNA. In the presence of the enzyme Q-beta replicase and suitable reaction conditions, preferred replicable RNAs are produced and act as a signal that such replicable RNA is present initially as sections A and F in the two detector-molecules and the reaction product in which it is incorporated.

A further embodiment of the present invention features a method of determining the presence or absence of a target molecule. The method comprises the steps of providing first and second detector-molecules. The first detector-molecule is a non-naturally occurring, recombinant RNA molecule capable of binding to a target analyte and has a structure

5'-A-B-C-3'.

The segments A, B and C are as previously described. The second detector molecule is a non-naturally occurring, recombinant RNA molecule capable of binding to the target analyte and has a structure:

5'-D-E-F-3'.

The sections D, E, F are previously described.

The method further comprises the step of imposing binding conditions on a sample potentially containing target molecules in the presence of the first and second detector-molecules. In the presence of the target molecule, the first and second detector molecules form a target first and second detector-molecule complex. The method further comprises the step of imposing RNA ligase reaction conditions on the sample to form a third RNA molecule in the presence of the target analyte. The third RNA molecule has the formula:

5'-A-B-C-D-E-F-3'.

The sample is monitored for the presence of the third RNA molecule, whose presence or absence indicates the presence or absence of the target analyte molecule.

Preferably, sections B and E bind to the target analyte through non-nucleic acid pairing interactions. And, most preferred, B and E are ligands demonstrating high affinity to separate epitopes of the same target analyte or they are parts of the same ligand that demonstrates high affinity to a single epitope of the target analyte.

Preferably, sections C and D are capable to serve as donor and acceptor captomers in the ligation reaction and can join covalently at the respective termini by the action of RNA ligase.

Preferably, at least one of the first or second detector-molecules has a signal-
5 generating moiety. Preferably, the non-signal-generating first and second detector-molecules are ligated and comprise a functioning, signal-generating template that can be amplified by Q-beta replicase. The analyte and the third RNA molecule are associated in the complex. All procedures of the binding of detector and analyte molecules and ligation of the detector molecules are performed according to the
10 standard protocols known to the someone skilled in the art of molecular biology.

A further embodiment of the present invention features the procedures essential for the elimination of possible background. The method preferably comprises the further step of hybridization of a specially designed primer with the complementary region of the C section prior to the template's amplification by Q-beta replicase. For
15 this hybridization, the mixture of detector-molecules annealed and non-annealed to the analyte are mixed with the primer that has complementary nucleotide sequences and can bind to a segment of the CD region of the ligated product. The mixture will be exposed to favorable conditions under which the primer will be reassociated with the complementary sequences of the CD region.

After primer reassociation conditions are imposed, the method preferably
20 comprises the further step of enzymatic degradation of the template molecules resulting from ligation of the first and second detector-molecules without binding to the analyte. Such molecules still bear the signal-generating moiety and, therefore, could be the source of background and false positive results. For this, the mixture will be
25 exposed to AML reverse transcriptase as was described earlier. Similarly, the enzyme with its dual function will synthesize cDNA complementary to the CD, E and F, or A and B regions depending on the plus or minus nature of the ligated product, and will simultaneously degrade these segments of the RNA template, eliminating the 5' portion of those template molecules not forming a complex with the target analyte.

30 After enzymatic degradation of the detector-molecules that are the ligation products of the first and second detector-molecules in the absence of the target analyte, the remaining templates are exposed to amplification by the Q-beta replicase enzyme.

A further embodiment of the present invention comprises a kit for determining the presence or absence of target molecules. The kit for identifying specific analytes in a specimen is composed of one or more reagents comprising the first and second detector-molecules specific for the desired or target analytes, RNA ligase, AML
5 reverse transcriptase, Q-beta replicase, primer for the reverse transcriptase, and buffers, salt and reagent solutions necessary to perform the experiments according to the designed protocol. The first detector molecules have the formula:

A-B-C.

The second detector molecules have a formula:

10 D-E-F.

All segments of the detector molecules are previously described.

A universal kit for constructing the detector molecules for any analyte of interest may be composed of one or more reagents comprising one of the RNA libraries, each species in which has a formula:

15 A-B-C-D-E-F.

The segments A, B, C, D, E and F are previously described. The kit also includes RNA ligase, AML reverse transcriptase, Q-beta replicase, a ribozyme that corresponds to the sequences in the CD region, primer for the reverse transcriptase, and buffers, salt and reagent solutions necessary to perform the experiments
20 according to the designed protocol.

It is possible to expect that some detector molecules will be ligated and will form template molecules without annealing with the analyte molecule. Elimination of the background created by these "accidental" templates will be accomplished by enzymatic degradation and will be performed prior to their amplification with Q-beta
25 replicase. A similar approach was used previously for differentiation of high and low affinity RNA recombinant molecules. After purifying the annealed detector molecule-target analyte complex from the DNA and RNA fragments, non-annealed target analytes and detector molecules, the intact template for Q-beta replicase, protected by the target analyte, will be separated from the target analyte. Amplifying the restored
30 template with Q-beta replicase will indicate the presence of even a small number of target analyte molecules in a specimen.

In a modification of this method to produce two detector-molecules, the recombinant DNA molecules are transcribed into RNA before the replication by Q-beta replicase. A RNA polymerase promoter is attached to the nonreplicable portion of the

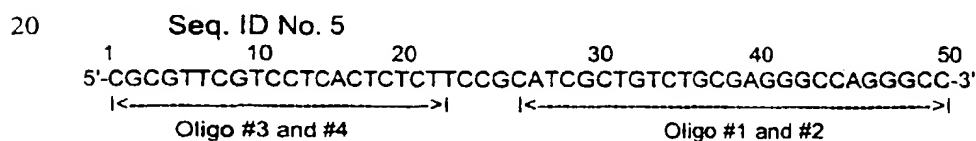
ligated detector-molecules before the transcription. The attachment of the promoter and transcription of recombinant RNA are used under the standard conditions known to someone skilled in the field of molecular biology.

EXAMPLE 1.

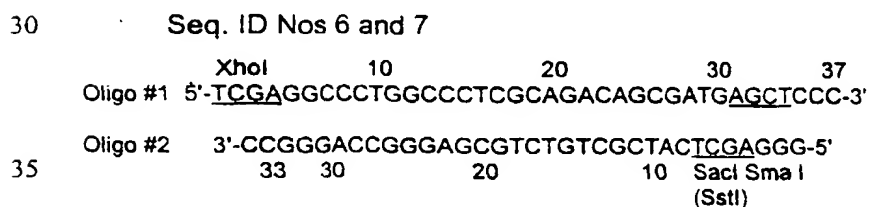
- 5 Using the above-cited specifics in the RNA ligase action, we performed an experiment in which the detector probes with captomers formed a "loose" ternary complex with a nucleic acid target and thus modeled a complex formed by the detector-probes with a protein target. We also investigated the ability of T4 RNA
ligase to use such a model complex as a substrate and to restore a template for Q-
10 beta replicase by joining specially-designed captomers.

Preparation of the detector probes.

- The fifty-base oligonucleotide sequence containing an Hha I- Pvu II region of the late promoter of adenovirus within map units 16.4 and 16.6 (Ziff and Evans, 1978)
15 was chosen as the model target in our experiments. It was synthesized on a DNA Synthesizer, together with two pairs of oligonucleotides—oligos #1 and #2 and oligos #3 and #4. The fifty base oligonucleotiding (Seq ID No 5) is described below with the position of Oligos, #1-4.



The first pair of oligos complement each other and represent the counterparts of the adenovirus target region from the nucleotide C²⁵ to the end of the sequence. Oligos #1 (Seq ID No. 6) and Oligo #2 (Seq ID No 7) are described below:



Both oligos have additional sequences representing the complete site for Sac I and a half for Sma I restriction enzymes, and the oligo #1 additionally has a sequence

of the Xho I restriction enzyme.

Oligos #3 and #4 represent the other half of the adenovirus target molecule and span from the beginning of the target sequence to the T²¹ base. Oligos #3 (Seq. ID No. 8) and Oligo #4 (Seq. ID No. 9) are described below:

5

Seq. ID Nos 8 and 9

	PpuM-I	10	20	22
Oligo #3	5'- <u>AAGAGAGT</u> GAGGACGAACGCGC-3'			
Oligo #4	3'- <u>TTCTCTCACTCCTGCTT</u> GCGCGAGCT-5'			
10	26	20	10	Xho I

Both oligos #3 and #4 have half of the recognition site for the PpuM-I restriction site and oligo #4 has a sequence of Xho I restriction enzyme, similar to oligo #1. These two pairs of oligos were also annealed and were used for cloning. They are referred to as the "PX fragment". These two pairs of oligos formed two dsDNA fragments, referred to as the "PX fragment" and "XS fragment". They were used for cloning in the recombinant plasmid pT7 MDV-XhoI.

Turning now to Fig. 1, which depicts plasmid pT7 MDV-XhoI, this plasmid was used for cloning of the synthesized PX and XS dsDNAs and for the transcription of the PX and XS recombinant RNA molecules that served as detector molecules for the adenovirus sequences. This plasmid is a variant of the parent plasmid, pT7 MDV, in which the XhoI linker sequence is not present. For further details of the construction of the vector, see Axelrod et al., 1991. A sequence described in Fig. 1 is designated Seq. ID No. 22.

The pT7MDV-Xho I plasmid DNA was digested either with Ppu MI and Xho I or with Sma I and Xho I restriction enzymes and purified from the excised 65 bp or 166 bp fragments of the cloned MDV cDNA insert. The remaining parts of the pT7MDV-XhoI plasmid after Ppu MI and Xho I digestion (pT7 MDV-1) contained the T7 promoter and 168 bp 3' end of the MDV cDNA. The remaining part of the pT7MDV-Xho I plasmid digested with Xho I and Sma I enzymes (pT7 MDV-2) contained T7 promoter and the 62 bp 5' end of the MDV cDNA. The PX fragment was ligated with the pT7 MDV-1 and the XS fragment was ligated with pT7 MDV-2, forming pPX and pXS recombinant plasmids. The presence of the two different cloning sites in the digested vector ensures only one possible orientation of the inserts in both the pPX and pXS plasmids. Each of these plasmids contains a T7RNA promoter, an insert

25

homologous to part of the target adenovirus sequence, and a segment of the MDV cDNA.

A control recombinant plasmid with target adenovirus DNA inserts was constructed as well. For this purpose, we modified the original adenovirus sequence so that it contained Xho I sites at both ends similarly to PX and XS fragments. The fragment was then inserted at the Xho I site of pT7 MDV- Xho I, creating plasmid p325. This plasmid was used either to produce the DNA target sequences or to synthesize the recombinant template MDV RNA with an insert of the adenovirus sequences.

Cold or ³²P-labeled RNA was transcribed from plasmids using T7RNA promoter after the Sma I digestion of pPX or p325 and Sst I or Sma I of pXS digestion according to the standard protocols (Sambrook et al., 1989)

The 193-base RNA transcript from the pPX plasmid is composed of (reading in the 5'→3' direction) the first three G residues of transcription initiation, 22 residues transcribed from the PX fragment and 168 residues transcribed from the 3' end of the MDV cDNA. This sequence (Seq. ID No. 10) is described below:

5'-GGG-AAGAGAGUGAGGACGAACGCGC-3' MDV-1 RNA (168 bases).

The RNA transcript from the pXS plasmid is only 92 bases, shorter than the pT7MDV-1 transcript, and it starts with the 62 residues of the 5' end MDV cDNA and is followed by the 30 residues transcribed from the XS fragment. This sequence (Seq. ID No. 11) is described below:

5'-MDV-1 RNA (62 bases)-GGCCCUGGCCCUCGCAGACAGCGAUGAGCU-3'.

An additional three C nucleotides were generated on 3' end of the XS recombinant RNA after Sma I digestion of the same plasmid.

These two recombinant RNAs represent a set of the PX and XS detector molecules. Each of these molecules has three functional parts: amplification, recognition and ligation.

Annealing experiments

PX detector was ³²P end-labeled to monitor the results of the annealing experiments. For this we used bacterial alkaline phosphatase (BAP) and

bacteriophage T4 polynucleotide kinase. Both reactions, dephosphorylation and end-labeling, were performed according to standard protocols (Sambrook et al., 1989). Incorporation of the radioactive label was measured in aliquots of the reaction and the percentages of incorporation were calculated.

5 The PX and SX detector molecules were hybridized with the target adenovirus oligonucleotide sequences. For this the three components were mixed in equal molarity proportion in a range of 2-3 pmole per reaction.

 The hybridization produces several radioactive bands, representing the products of association between the target adenovirus DNA and the PX and XS
10 probes.

 The annealing reaction products between the PX and XS detector-molecules and adenovirus target sequences were characterized. PX recombinant RNA was ³²P end-labeled using standard methods. Annealing was achieved by boiling the reaction mix two minutes and then incubating it at 65°C for two hours. The annealing reaction
15 was carried out in a solution containing 50 mM TRIS pH 7.8, 5 mM MgCl₂, 0.5 mM ATP and 1 mM EDTA, 10% non-denaturing PAGE at 500 volts for eight hours.

 The most plausible explanation of the results is that a top band results from the annealing of the target DNA molecule with both RNAs. Such complex is composed of from 50 bp double stranded heteroduplex of target/probes segment and 168 bases 3'-
20 end and 62 bases 5'-end of MDV-I. A lowest band is 193 nucleotides of non-hybridized PX RNA and one of the middle bands, with a size of 243 bases, is a complex between PX RNA and adenovirus DNA molecules. The origin of a second band of similar size is unknown.

 The efficiency of hybridization was calculated as a percentage of the
25 radioactivity of the top band from the total radioactivity applied on the gel. Usually more than 50% of the total number of PX RNA molecules participate in hybridization with the adenovirus target molecule by itself or in compound with XS. The yield of the ternary complex formed by two RNA detector molecules and the target molecules was, usually, close to 30-40%.

30 Fig. 2 illustrates a possible hybridization configuration between the target adenovirus sequence and the two RNA transcripts. The SX RNA detector, in this case, was generated by Sst I digestion of the pSX plasmid. The ligated first and second RNA molecules are identified in Seq. ID No. 12.

There is complete complementarity along the PX RNA detector and the first 23 bases of the target molecule, but not the last, the 24th G-residue of the transcript and the G-base of the adenovirus target molecule. The first four bases of the XS detector (UCGA) do not have homologous nucleotides on the target DNA molecule, although
5 the rest of the transcript is complementary to the target molecule. Thus, the hybridized RNA transcripts do not juxtapose to the target end-to-end fashion, but rather leave a ~20 Angstrom gap between the terminal hybridized nucleotides.

The G and UCGA nucleotides of the PX and XS detector probes are the captomers. They do not hybridize to the target and comprise structures similar to the
10 donor/acceptor complex, which is necessary in order for RNA ligase to form a phosphodiester bond (Uhlenbeck, 1983). The G captomer is a donor with a 5'-phosphate terminus and the UCGA captomer is an acceptor with a 3'-hydroxyl terminal group on the U residue.

15 Ligation experiments

The recombinant plasmid pXS was constructed in a such way that it could be linearized either with SmaI or SstI for RNA transcription. The two XS RNA detector molecules are different in the total lengths and composition of their captomers. The XS detector generated with Sst I digestion had a captomer of four UCGA-base-long
20 bases, whereas the captomer generated after the Sma I digestion was longer for the three Cs.

Ligation reactions were carried out on 4 ul aliquots taken directly from the annealing reactions in the presence of the 10nM mercaptoethanol, and 40 Units of T4 RNA ligase at 25°C after confirmation by gel electrophoresis that hybridization was
25 successful. The duration of the reaction varied from 2 hours to overnight. The bands representing ligation product composed of PX-SX ligated detector molecules were excited and their radioactivity was measured and compared with the total radioactivity of the aliquot from the annealing reaction used for the ligation. The total volume of each ligation reaction was 10 ul, with the final concentrations 10 mM, 5 mM MgCl₂ and
30 2 Units of T4 RNA ligase in the presence of 20% PEG. The reaction was performed at 25°C and ended by adding 1 ul of 100 mM EDTA, 7M Urea denatured 10% PAGE at 500 volts for eight hours of electrophoresis.

Additionally, the duration of the reaction apparently does not affect the rate of ligation when the long captomers were used. The yield of the ligated product was

20.0 % after two hours of reaction and 18.7% after overnight. The longer reaction time, however, might have a certain disadvantage when the short captomers are used. The overnight reaction yielded 18.4% compared with 33.2% after two hours of reaction. The reduction in the percentages of ligated products after a prolonged
 5 reaction time apparently indicate that the ligation products composed of PX and XS RNA transcripts are not stable and dissociate over time. The results of the ligation experiment demonstrates that the length of the XS captomer seemingly does not effect the ligation rate of the RNA transcripts, although the highest ligation rate was observed when the acceptor-captomer was composed of the seven-AGCUCCC-
 10 residues. ³²P-labeled recombinant MDV-I RNA, with the adenovirus insert transcribed from the p325 plasmid, served as a reference marker.

Table 1. Effect of the captomer's length on the yield of the ligation products between PX and XS RNA transcripts. 4 ul aliquots of the annealing reactions (1-6*) with two RNA transcripts and adenovirus target DNA were used for the subsequent
 15 ligation reaction. 4 ul aliquots of the annealing reaction (7**) without the target DNA were used as the negative control.

Test #	Length of captomer used in the	Duration of reaction at 25°C	Total counts (cpm) of the band in the gel reaction	Their proportion (%) from the counts loaded
20	1. Short ¹	2 hours	3428	20.0%
	2. Short	o/n	3140	18.7%
25	3. Long ²	2 hours	5576	33.2%
	4. Long	2 hours	1657	9.9%
	5. Long	o/n	3085	18.4%
	6. Long	o/n	1385	8.2%
	7. Long	2 hours	98	0.01%

30

*— 16.800 cpm were loaded into each test lane

**— 76.700 cpm were loaded into a control lane

The short (UCGA) captomer was generated by the pXS plasmid DNA digestion by the Sst I restriction enzyme, and the long (AGCUCCC) captomer resulted from the
 35 digestion of the pXS plasmid DNA by the Sma I restriction enzyme.

The ligation product composed of the ligated PX and XS RNA detector molecules was purified by gel electrophoresis. The purified product was used as a template for Q-beta replicase.

5 Amplification of the ligation products by Q-beta replicase

Q-beta replicase reactions were carried out on a volume of 20 μ l at 37°C during 25-30 minutes in 50- μ l reactions containing 88 mM Tris-HCL (pH 7.5), 12 mM MgCl₂, 0.2 mM of each ribonucleoside triphosphate, 25 μ Ci of [alpha-³²P]GTP, 90 pm/ml of Q-beta replicase, and 11.2 pm/ml of template RNA. From this mixture, 7 to 15 μ l was
10 applied directly onto a denaturing polyacrylamide gel containing 7M Urea for electrophoretic analysis. Additionally, adsorbed radioactivity was determined by liquid scintillation.

The Q-beta replicase experiment demonstrates that there are no templates for Q-beta enzyme in the aliquots representing the tube in which the ligation was
15 performed without the adenovirus target, which indicate that target analyte was necessary to unite two detector probes. A ligation reaction was performed on aliquots of the annealing reaction. The 5 μ l aliquots from each reaction were analyzed on a non-denaturing gel.

The obtained data suggest that amplification of the template by Q-beta
20 replicase occurred only when ligation of the PX and XS RNA detector molecules took place in the presence of the target.

The present invention features a >flexible= detector-target ternary complex and captomers sections. These features permit use of RNA ligase to restore the ability of recombinant MDV-1 RNA to be a template for Q-beta replicase.

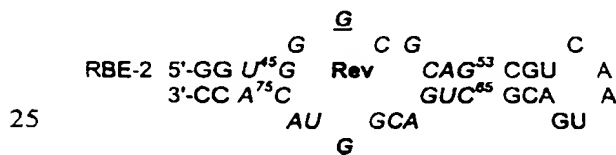
25

EXAMPLE 2.

A Q-beta replicase-based system of detector-molecules can be constructed and used to identify a protein target in a clinical specimen. As an example we use the high affinity RNA ligand (RRE-aptamer) for Rev protein. The central role of Rev
30 protein in primary and reactivated human immunodeficiency virus type 1 (HIV-1) infections is well studied. The interaction of Rev protein and the cis-acting Rev Responsive Element (RRE) is required for cytoplasmic accumulation of HIV structural proteins encoding viral mRNAs (Malim et al., 1989). The Rev protein has been isolated and purified and a series of high affinity aptamers have been identification.

The structure of RRE and the mechanism of interaction between RRE aptamers and Rev protein is well studied. (Karn et al., 1991). The RRE and its aptamers consist of three functional parts. One "bubble" (the core region), and two double-stranded stems that flank the core region. Experiments with nucleotide substitution showed that the annealing abilities of the whole aptamer depends on the existence of a core region, its nucleotide composition and tertiary configuration. The nucleotide composition of the flanking stems is not crucial as long as the stems ensure the existence of the core region (Giver et al., 1993 a, b). SELEX-derived oligonucleotides with K_d are about 10 times lower than those of wild type RRE (Giver et al. *ibid.*). Therefore, RRE aptamers can successfully compete with native RRE for the Rev protein. The Rev protein system and high affinity RNA ligands selected *in vitro* are used by many research groups as targets for designing an anti-HIV structure-based drug (Klug and Famulok, 1994).

RBE-2, a high affinity aptamer selected through SELEX, preserves the structure of the RRE core element, which is supported by two double-stranded stems, and demonstrates high affinity to Rev protein (Bartel et al., 1991). The nucleotides in the core region $U^{45} \rightarrow G^{53}$ and $C^{65} \rightarrow A^{75}$, which are involved in the binding motif for Rev recognition, are shown in italics in the diagram below. A major groove formed in the core region by the two G bases, is underlined and bold in the diagram. The sequence is identified as Seq. ID No. 13.



30 These two nucleotides open or pull apart the otherwise stringed stem of complementary nucleotides. Such widening is necessary for precise spatial positioning of the Rev peptide's "epitope" in the major groove. Finally, hydrogen bonds form between the Rev protein and RNA, securing a tight and specific binding into the complex (Iwai et al., 1992).

To construct recombinant RNA molecules containing the aptamer sequences for Rev protein and sequences for the template for Q-beta replicase, the dsDNA representing the whole aptamer with terminal XhoI sites, and the two dsDNAs representing the halves of the aptamer, are synthesized. These, too, will have appropriate cloning restriction site terminals. The three oligonucleotides are cloned in

31

a pT7 MDV-Xho I plasmid (Fig. 1), using the same strategy and procedures that were performed in model experiments with detector probes specific for the adenovirus sequences. A dsDNA (Seq. ID Nos. 14 and 19) corresponding to a first aptamer is depicted below:

5 Seq ID Nos. 14 and 19

Rev protein aptamer 5'--TCGA--GGTGGGCGCAGCGTCAATGACGCTGACGGTACACC--3'
 dsDNA 3'--CCACCCGCGTCGCAGTTACTGCGACTGCCATGTGG--AGCT--5'
 XhoI XhoI

10 A second dsDNA (Seq. ID Nos. 15 and 20) corresponding to a second aptomer is described below:

Seq ID Nos. 15 and 20

15 dsDNA of first 5'--TCGA--GGTGGGCGCAGCGTCAA--AGCT--3'
 detector molecule 3'--CCACCCGCGTCGCAGTT--TCGA--5'
 SstI

A third dsDNA (Seq. ID No. 16 and 21) corresponding to a third aptomer is described below:

20 Seq ID Nos. 16 and 21

dsDNA of second 5'--AA--TGACGCTGACGGTACACC--3'
 detector molecule 3'--TT--ACTGCGACTGCCATGTGG--AGCT--5'
 PpuMI XhoI

25

RNA detector probe transcripts, composed of the RBE-2 and Q-beta replicase template sequences, will be synthesized for each pair of oligos, similar to those of the PX and XS for adenovirus, using the T7 RNA promoter and T7RNA polymerase. The composition of the recombinant RNA transcripts representing the two recombinant

30 RNA detector molecules (Seq. ID No. 17 and 18) are described below:

5'--62ntMDV--GGUGGGCGCAGCGUCAA--AGCU--3'
 5'--GGG--AA--UGACGCUGACGGUACACC--168ntMDV--3'

35 The Fig. 3a demonstrates the possible configuration of the ternary Rev protein-detector probes complex. The detector molecules would be ligated with T4 RNA ligase and will form a single molecule as shown in Fig 3b and described in the Sequence Listing as Seq ID No. 23.

40 The newly constructed aptamer is different from the original by the elongation of the stem between the core region by two base pairs and the loop by five bases.

32

and by the presence of MDV RNA sequences. Its composition is 5'-62ntMDV-RBE-2-168ntMDV-3'. It will be released in a low-salt buffer and MDV reporter templates can be amplified with Q-beta replicase without any additional processing. The number of reporting ligated detector molecules presented in the eluted sample will be

- 5 proportional to the number of Rev protein molecules in the model samples or clinical specimens, and can be estimated by adding the sample to a standard reaction mixture at 37°C containing Q-beta replicase and measuring the time required to produce a signal with an intercalating fluorescent dye. Appropriate negative and positive standards will be tested simultaneously with the specimens to establish sensitivity and
- 10 specificity levels of the assay and to find a correlation between the assay results and the actual HIV titer in the clinical specimens. On the serially diluted Rev protein samples, we will establish a relationship between response time and the number of target molecules in the sample. The response time is universally proportional to the log of the number of template molecules present in the sample (Lomeli et al., 1989).
- 15 The fluorescence of the amplified detector molecules will be photographed over an ultraviolet light box or measured in a fluorometer. The results of these experiments will enable us to identify the conditions necessary to form the preferred ternary complex of Rev protein and recombinant RNA detector probes with minimal background for the whole assay and, therefore, with high specificity for the whole
- 20 assay.

Thus, while preferred embodiments have been illustrated and described, it is understood that the present invention is capable of variation and modification and therefore, should not be limited to the precise details set forth, but should include such changes and alterations that fall within the purview of the following claims.

25

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SEQUENCE LISTING

(i) APPLICANT:

- (A) ADDRESSEE: InVitro Diagnostics, Inc.
- (E) STREET: 666 Washington Avenue
- (C) CITY: Pleasantville
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 10570

(ii) TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF TARGET MOLECULES

(iii) NUMBER OF SEQUENCES: 23

(iv) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT Unassigned
- (B) FILING DATE: Concurrently Herewith

(v) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/801,154
- (B) FILING DATE: 18-FEB-1997

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGGACCCCC CCGGAAGGGG GGGACGAGGU GCGGGCACCU CGUACGGGAG JUCGACCGUG . 60
ACGCUCUAG 69

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGAUCUAGAG CACGGGCUAG CGCUUUCGGG CUCUCCCAGG UGACGCCUCG UGAAGAGGCG 60
CGACCUUCGU GCGUUUCGGU GACGCACGAG AACCGCCACG CUGCUUCGCA GCGUGGCUCC 120
UUCGCGCAGC CCGCUGCGCG AGGUGACCCC CCGAAGGGGG GUUCCC 166

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGGAAAUCC UGUUACCAGG AUAACGGGGU UUCCUCA 37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCUCUCUACU CGAAAGUUAG AGAGGACACA CCCGGAUCUA GCCGGGUCAA CCA 54

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCGTTCGTC CTCACTCTCT TCCGCATCGC TGTCTGCGAG GGCCAGGGCC 50

(2) INFORMATION FOR SEQ ID NO:6:

37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCGAGGCCCT GGCCCTCGCA GACAGCGATG AGCTCCC

37

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGAGCTCAT CGCTGTCTGC GAGGGCCAGG GCC

33

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGAGAGTGA GGACGAACGC GC

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

38

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGAGCGCGT TCGTCCTCAC TCTCTT

26

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAAGAGAG UGAGGACGAA CGCGC

25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCCUGGCC CUCGCAGACA GCGAUGAGCU

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCCCUGGCC CUCGCAGACA GCGAUGAGCU GGGGAAGAGAG UGAGGACGAA CGCG

54

(2) INFORMATION FOR SEQ ID NO:13:

39

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGUGGGCGCA GCGUCAAUGA CGCUGACGGU ACACC

35

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGAGGTGGG CGCAGCGTCA ATGACGCTGA CGGTACACC

39

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGAGGTGGG CGCAGCGTCA AAGCT

25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGACGCTG ACGGTACACC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGUGGGCGCA GCGUCAAAGC U

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGAUGACG CUGACGGUAC ACC

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGAGGTGTA CGTCAGCGT CATTGACGCT GCGCCCACC

39

(2) INFORMATION FOR SEQ ID NO:20:

41

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iv) ANTI-SENSE: YES

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTTGACG CTGCGCCAC C

21

- (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: RNA

- (iv) ANTI-SENSE: YES

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCGAGGTGTA CCGTCAGCGT CATT

24

- (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTTGGGCT GCAGGTCTAA TACGACTCAC TATAGGGGAC CCCCCGAGTC CTCGAGGAGT

60

CACCCCGGGA ATT

73

- (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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42

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGUGGGCGCA GCGUCAAAGC U

21

IN THE CLAIMS

1. A first ribonucleic acid (RNA) molecule and a second RNA molecule for use in determining the presence or absence of a target molecule, said first RNA molecule
5 capable of binding to a target molecule and having the following formula:

5'-A-B-C-3';

- wherein A is a section of the RNA molecule having 10-100,000 nucleotides which
10 section is capable of being received by an RNA replicase and with another RNA sequence, F, being replicated and the letter "B" denotes a section of the RNA molecule having approximately 10 to 50,000 nucleotides which section is capable of binding to the target molecule and the letter "C" denotes a section of the RNA molecule having approximately 1 to 10,000 nucleotides which section is capable of
15 being ligated to another RNA sequence, "D"; said second RNA molecule capable of binding to said target molecule and having the following formula:

5'-D-E-F-3';

- 20 wherein D is a section of the RNA molecule having approximately 1 to 10,000 nucleotides which section is capable being ligated with another RNA sequence, "C", and the letter "E" denotes a section of the RNA molecule having approximately 10 to 100,000 nucleotides which section is capable of binding to the target molecule, and the letter "F" denotes a section of the RNA molecule having 10 to 100,000 nucleotides
25 which section is capable of being received by an RNA replicase and with another sequence, "A", being replicated; said first and the second RNA molecules are capable of forming a third RNA molecule having the following formula:

5'-A-B-C-D-E-F-3';

30

said third RNA molecule formed by ligating the C and D sections, as the E and the B sections are bound to target, said third RNA molecule capable of being received by an RNA replicase and being replicated by such enzyme as a indication of the presence or absence of the target molecule.

2. The RNA molecules of claim 1 wherein said sequences represented by the letters "A" and "F" are selected from the group of sequences consisting of MDV-I RNA, Q-beta RNA microvariant RNA, nanovariant RNA, midvariant RNA and modifications of such sequences which maintain the ability of the sequences to be replicated by Q-beta replicase.
3. The RNA molecules of claim 1 wherein the sections B and E bind to the target through non-nucleic acid pairing interactions.
4. The RNA molecules of claim 4 wherein the B and E sections are aptamers or partial aptamers.
5. The RNA molecules of claim 1 wherein the sections C and D together define a site for ligation.
6. A method of determining the presence or absence of a target molecule, said method comprising the following steps:
- a.) providing a first RNA molecule and a second RNA molecule of any claim 1-5;
 - b.) combining a sample potentially containing the target molecule with said first and said second RNA molecules and imposing conditions which allow said first and said second RNA molecules and said target molecule to form a first second RNA molecule target complex;
 - c.) imposing RNA ligase conditions on said sample to form said third RNA molecule in the presence of the target molecule;
 - d.) imposing amplification conditions on said sample to form an amplification product in the presence of target; and
 - e.) monitoring the sample for the presence or absence of the third RNA molecule as indicative of the presence or absence of the target molecule.
7. The method of claim 6 further comprising the step of removing first and second RNA molecules which do not form a complex.

45

8. The method of claim 7 wherein said first and second RNA molecules which do not form a complex are enzymatically destroyed.

9. The method of claim 6 wherein said amplification conditions comprise combining
5 said sample potentially containing said third RNA molecule with the enzyme Q-beta replicase.

10. A kit for determining the presence or absence of a target molecule comprising a first ribonucleic acid (RNA) molecule and a second RNA molecule as described in any
10 one claims 1-5, ligase means and amplification means.

11. A method of making a first ribonucleic acid (RNA) molecule and a second RNA molecule as described in any claim 1-5 for use in determining the presence or absence of a target molecule; comprising the step of combining a sample containing
15 the target molecule with a library of RNA molecules having the formula:



to form a mixture of one or more target bound RNA molecules and one or more
20 unbound RNA molecules, wherein the letters B' and E' are sections with randomized nucleotides and represent potential sections B and E; and performing at least one step i or ii as set forth below:

i) combining primer nucleic acid corresponding to at least one section with the mixture with an enzyme capable of degrading the unbound RNA molecules and
25 imposing conditions for degradation; releasing said bound RNA molecules from target; and amplifying said bound RNA molecules with an RNA replicase to form an amplification product having the formula:



30 or;

ii) amplifying the bound RNA in situ or after releasing said bound RNA molecules from target to form an amplification product having the formula:



and;

cleaving said amplification product to form the first and second RNA molecules.

12. The method of claim 11 wherein said sections B' and E' are randomized nucleotide sequences.

5

13. The method of claim 11 wherein said step ii is followed by serial dilution of the amplification product and repeated to identify the amplification product with highest affinity and greatest amplification potential.

10 14. A kit for performing the method of claim 11-13 comprising one or more sections of the third RNA molecule and an amplification enzyme.

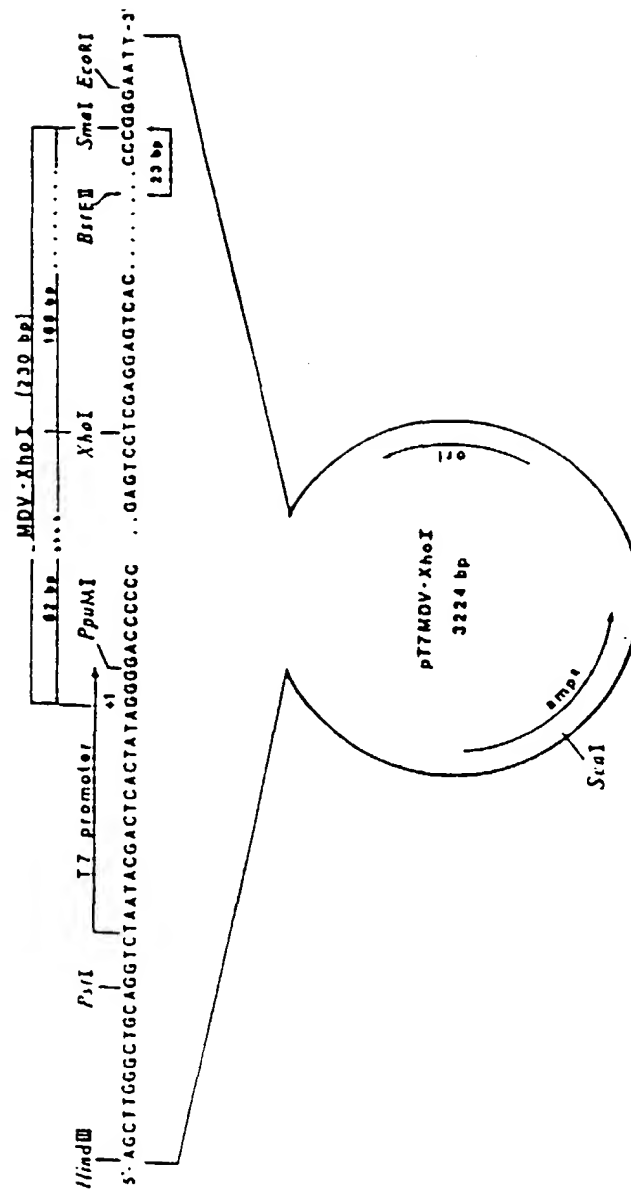


FIG. 1

2/2

```

1      10      20      24      30      40      50
CGCGTTCGTCCTCACTCTCTTCC-G-CATCGCTGTCTGCGAGGGCCAGGGCC
GCGCAAGCAGGAGUGAGAGAAGG  GUAGCGACAGACGCUCCCGUCCCGG
(PX detector molecule G   A   XS detector molecule)
      U-C-G
168 bases of MDV-1 RNA-3'  5'-62 bases of MDV-1 RNA

```

FIG. 2

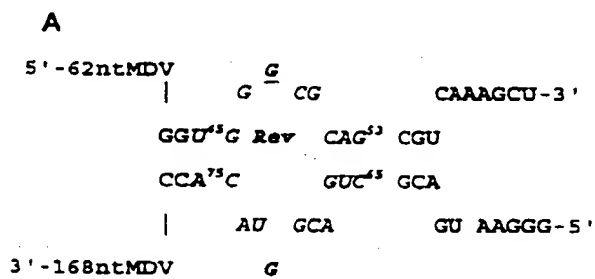


FIG. 3A

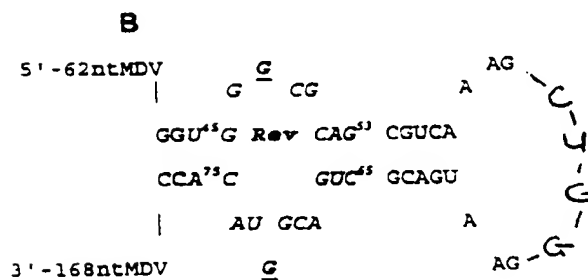


FIG. 3B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/03210

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/68; C07H 21/02
US CL : 435/6, 91.2, 91.21; 536/24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.2, 91.21; 536/24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5,407,798 A (MARTINELLI et al.) 18 April 1995, see entire document.	1-3, 5-14
Y		4
Y	US 5,582,981 A (TOOLE et al.) 10 December 1996, especially columns 1 and 2.	3

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

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O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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Date of the actual completion of the international search

24 APRIL 1998

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